

SEQUENCE LISTING

<110> Thomas, Christopher
McPherson, Michael
Atkinson, Howard
Neelam, Anil

<120> Plant Cell Death System

<130> 9341-028

<150> 0025225.4

<151> 2000-10-14

<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 945

<212> DNA

<213> *Phytolacca americana*

<220>

<221> mutation

<222> (750)..(759)

<223> Sequence replacing removed XbaI site

<220>

<221> misc_feature

<222> (1)..(24)

<223> Binding site for primer PPS1BF

<220>

<221> misc_feature

<222> (736)..(777)

<223> Binding site for primer PSXDF

<220>

<221> misc_feature

<222> Complement((735)..(776))

<223> Binding site for primer PSXDR

<220>

<221> misc_feature

<222> Complement((922)..(945))

<223> Binding site for primer PPS2SR

<400> 1

atgaagggtga tgctttagt tgtggtgacg ttaatagcgt ggctcattgc tgcaccaact 60

tcaacttggtg ccataaatac gatcaccttt gatgctggaa atgccaccat taacaaatat 120

gccaccttta tggaatctct tcgtaatcaa gcgaaagatc caaaactaaa atgctatggc 180

ataccaatgc tacctgatac taattogacc cctaagtact tattgggttaa gtcceaaggt 240

gcaaacctaa aaaccattac actaatgctg agacgaaata acttatacgt gatgggctat 300

tctgatccct tcaatggcaa taagtgtcgt taccatatat ttaatgatat tacaagcacc 360
gaacgcactg atgtggagaa tactctttgc tcaagttcta gttctcgtgt tgcaatgtcc 420
attaactaca atagcttata tccgaccatg gaaaagaaag cagaagtaaa ctcaagaaat 480
caagtccaat tgggaattca aatactcagc agtgacattg gaaaaatctc tggagttgat 540
tcattccctg taaaaactga ggcttttttt ctactggtag ccatccaaat ggtttcagag 600
gcagcgcgat tcaagtacat agagaaccaa gtcaagacta attttaatag agcattctac 660
cctgatccca aagtaattaa tttggaggag aagtggggca aaatctctga ggcaattcac 720
aatgccaaga atgggggcttt acccaaacca cttgagctag tggatgcaa aggtaccaag 780
tggatagttc ttagagtgga tgaaatcaat cgtgatgtgg cactccttaa gtacgttaat 840
ggaacctgtc agacaactta caaaatgcc atgttctctc aagttataat ttctacttat 900
tataattata tgtctaactc tggatgata tttgaaggat tctaa 945

<210> 2

<211> 314

<212> PRT

<213> *Phytolacca americana*

<220>

<221> PROPEP

<222> (1) .. (24)

<223> N-terminal processed segment

<220>

<221> PROPEP

<222> (287) .. (314)

<223> C-terminal processed segment

<400> 2

Met Lys Val Met Leu Val Val Val Val Thr Leu Ile Ala Trp Leu Ile
1 5 10 15

Ala Ala Pro Thr Ser Thr Cys Ala Ile Asn Thr Ile Thr Phe Asp Ala
20 25 30

Gly Asn Ala Thr Ile Asn Lys Tyr Ala Thr Phe Met Glu Ser Leu Arg
35 40 45

Asn Gln Ala Lys Asp Pro Lys Leu Lys Cys Tyr Gly Ile Pro Met Leu
50 55 60

Pro Asp Thr Asn Ser Thr Pro Lys Tyr Leu Leu Val Lys Leu Gln Gly
65 70 75 80

Ala Asn Leu Lys Thr Ile Thr Leu Met Leu Arg Arg Asn Asn Leu Tyr
85 90 95

Val	Met	Gly	Tyr	Ser	Asp	Pro	Phe	Asn	Gly	Asn	Lys	Cys	Arg	Tyr	His	100	105	110	
Ile	Phe	Asn	Asp	Ile	Thr	Ser	Thr	Glu	Arg	Thr	Asp	Val	Glu	Asn	Thr	115	120	125	
Leu	Cys	Ser	Ser	Ser	Ser	Ser	Arg	Val	Ala	Met	Ser	Ile	Asn	Tyr	Asn	130	135	140	
Ser	Leu	Tyr	Pro	Thr	Met	Glu	Lys	Lys	Ala	Glu	Val	Asn	Ser	Arg	Asn	145	150	155	160
Gln	Val	Gln	Leu	Gly	Ile	Gln	Ile	Leu	Ser	Ser	Asp	Ile	Gly	Lys	Ile	165	170	175	
Ser	Gly	Val	Asp	Ser	Phe	Pro	Val	Lys	Thr	Glu	Ala	Phe	Phe	Leu	Leu	180	185	190	
Val	Ala	Ile	Gln	Met	Val	Ser	Glu	Ala	Ala	Arg	Phe	Lys	Tyr	Ile	Glu	195	200	205	
Asn	Gln	Val	Lys	Thr	Asn	Phe	Asn	Arg	Ala	Phe	Tyr	Pro	Asp	Pro	Lys	210	215	220	
Val	Ile	Asn	Leu	Glu	Glu	Lys	Trp	Gly	Lys	Ile	Ser	Glu	Ala	Ile	His	225	230	235	240
Asn	Ala	Lys	Asn	Gly	Ala	Leu	Pro	Lys	Pro	Leu	Glu	Leu	Val	Asp	Ala	245	250	255	
Lys	Gly	Thr	Lys	Trp	Ile	Val	Leu	Arg	Val	Asp	Glu	Ile	Asn	Arg	Asp	260	265	270	
Val	Ala	Leu	Leu	Lys	Tyr	Val	Asn	Gly	Thr	Cys	Gln	Thr	Thr	Tyr	Gln	275	280	285	
Asn	Ala	Met	Phe	Ser	Gln	Val	Ile	Ile	Ser	Thr	Tyr	Tyr	Asn	Tyr	Met	290	295	300	
Ser	Asn	Leu	Gly	Asp	Leu	Phe	Glu	Gly	Phe							305	310		

<210> 3

<211> 792

<212> DNA

<213> *Phytolacca americana*

<220>

<221> mutation

<222> (612)

<223> Nucleotide change from published sequence

<220>

<221> mutation

<222> (681)..(686)

<223> Sequence replacing removed XbaI site

<220>
 <221> misc_feature
 <222> (1)..(3)
 <223> Initiation codon added via PCR primer

<220>
 <221> misc_feature
 <222> (790)..(792)
 <223> Stop codon added via PCR primer

<220>
 <221> misc_feature
 <222> (1)..(29)
 <223> Binding site for primer PS1BF

<220>
 <221> misc_feature
 <222> Complement((765)..(792))
 <223> Binding site for primer PS2SR

<220>
 <221> misc_feature
 <222> Complement((436)..(462))
 <223> Binding site for primer PS1SR

<220>
 <221> misc_feature
 <222> (463)..(492)
 <223> Binding site for primer PS2BF

<400> 3
 atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt 60
 atggaatctc ttcgtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg 120
 ctacctgata ctaattcgac ccctaagtac ttattgggta agtccaagg tgcaaaccta 180
 aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc 240
 ttcaatggca ataagtgtcg ttaccatata tttaatgata ttacaagcac cgaacgcact 300
 gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac 360
 aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa 420
 ttgggaattc aaatactcag cagtgacatt ggaaaaatct ctggagttga ttcattccct 480
 gtaaaaaactg aggctttttt tctactggta gccatccaaa tggtttcaga ggcagcgcg 540
 ttcaagtaca tagagaacca agtcaagact aattttaata gagcattcta cctgatccc 600
 aaagtaatta acttggagga gaagtggggc aaaatctctg aggcaattca caatgccaa 660
 aatggggctt tacccaaacc acttgagcta gtggatgcca aaggtaccaa gtggatagtt 720
 cttagagtgg atgaaatcaa tcgtgatgtg gcactcctta agtacgttaa tggaacctgt 780

<210> 4

<211> 263

<212> PRT

<213> *Phytolacca americana*

<400> 4

Met Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile Asn Lys
 1 5 10 15

Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp Pro Lys
 20 25 30

Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser Thr Pro
 35 40 45

Lys Tyr Leu Leu Val Lys Leu Gln Gly Ala Asn Leu Lys Thr Ile Thr
 50 55 60

Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro
 65 70 75 80

Phe Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Thr Ser
 85 90 95

Thr Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser Ser Ser
 100 105 110

Arg Val Ala Met Ser Ile Asn Tyr Asn Ser Leu Tyr Pro Thr Met Glu
 115 120 125

Lys Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly Ile Gln
 130 135 140

Ile Leu Ser Ser Asp Ile Gly Lys Ile Ser Gly Val Asp Ser Phe Pro
 145 150 155 160

Val Lys Thr Glu Ala Phe Phe Leu Leu Val Ala Ile Gln Met Val Ser
 165 170 175

Glu Ala Ala Arg Phe Lys Tyr Ile Glu Asn Gln Val Lys Thr Asn Phe
 180 185 190

Asn Arg Ala Phe Tyr Pro Asp Pro Lys Val Ile Asn Leu Glu Glu Lys
 195 200 205

Trp Gly Lys Ile Ser Glu Ala Ile His Asn Ala Lys Asn Gly Ala Leu
 210 215 220

Pro Lys Pro Leu Glu Leu Val Asp Ala Lys Gly Thr Lys Trp Ile Val
 225 230 235 240

Leu Arg Val Asp Glu Ile Asn Arg Asp Val Ala Leu Leu Lys Tyr Val
 245 250 255

Asn Gly Thr Cys Gln Thr Thr
260

<210> 5
<211> 465
<212> DNA
<213> *Phytolacca americana*

<220>
<221> misc_feature
<222> (1)..(3)
<223> Initiation codon added via PCR primer

<220>
<221> misc_feature
<222> (462)..(465)
<223> Stop codon added via PCR primer

<400> 5
atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt 60
atggaatctc ttcgtaatca agcgaaagat ccaaaactaa aatgctatgg cataccaatg 120
ctacctgata ctaattcgac ccctaagtac ttattgggta agtccaagg tgcaaacta 180
aaaaccatta cactaatgct gagacgaaat aacttatacg tgatgggcta ttctgatccc 240
ttcaatggca ataagtgtcg ttaccatata ttaatgata ttacaagcac cgaacgcact 300
gatgtggaga atactctttg ctcaagttct agttctctgtg ttgcaatgtc cattaaactac 360
aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa 420
ttgggaattc aaatactcag cagtgacatt ggaaaaatct cttaa 465

<210> 6
<211> 154
<212> PRT
<213> *Phytolacca americana*

<400> 6
Met Ile Asn Thr Ile Thr Phe Asp Ala Gly Asn Ala Thr Ile Asn Lys
1 5 10 15
Tyr Ala Thr Phe Met Glu Ser Leu Arg Asn Gln Ala Lys Asp Pro Lys
20 25 30
Leu Lys Cys Tyr Gly Ile Pro Met Leu Pro Asp Thr Asn Ser Thr Pro
35 40 45
Lys Tyr Leu Leu Val Lys Leu Gln Gly Ala Asn Leu Lys Thr Ile Thr
50 55 60
Leu Met Leu Arg Arg Asn Asn Leu Tyr Val Met Gly Tyr Ser Asp Pro
65 70 75 80

Phe Asn Gly Asn Lys Cys Arg Tyr His Ile Phe Asn Asp Ile Thr Ser
85 90 95

Thr Glu Arg Thr Asp Val Glu Asn Thr Leu Cys Ser Ser Ser Ser Ser
100 105 110

Arg Val Ala Met Ser Ile Asn Tyr Asn Ser Leu Tyr Pro Thr Met Glu
115 120 125

Lys Lys Ala Glu Val Asn Ser Arg Asn Gln Val Gln Leu Gly Ile Gln
130 135 140

Ile Leu Ser Ser Asp Ile Gly Lys Ile Ser
145 150

<210> 7
<211> 333
<212> DNA
<213> *Phytolacca americana*

<220>
<221> misc_feature
<222> (1)..(3)
<223> Initiation codon added via PCR primer

<220>
<221> misc_feature
<222> (331)..(333)
<223> Stop codon added via PCR primer

<400> 7
atgggagttg attcattccc tgtaaaaact gagggcttttt ttctactggt agccatccaa 60
atgggtttcag aggcagcgcg attcaagtac atagagaacc aagtcaagac taattttaat 120
agagcattct accctgatcc caaagtaatt aatttggagg agaagtgggg caaaatctct 180
gaggcaattc acaatgcaa gaatggggct ttacccaaac cacttgagct agtggatgcc 240
aaaggtagca agtggatagt tcttagagt gatgaaatca atcgtgatgt ggcactcctt 300
aagtacgtta atggaacctg tcagacaact taa 333

<210> 8
<211> 110
<212> PRT
<213> *Phytolacca americana*

<400> 8
Met Gly Val Asp Ser Phe Pro Val Lys Thr Glu Ala Phe Phe Leu Leu
1 5 10 15

Val Ala Ile Gln Met Val Ser Glu Ala Ala Arg Phe Lys Tyr Ile Glu
20 25 30

Asn Gln Val Lys Thr Asn Phe Asn Arg Ala Phe Tyr Pro Asp Pro Lys
 35 40 45
 Val Ile Asn Leu Glu Glu Lys Trp Gly Lys Ile Ser Glu Ala Ile His
 50 55 60
 Asn Ala Lys Asn Gly Ala Leu Pro Lys Pro Leu Glu Leu Val Asp Ala
 65 70 75 80
 Lys Gly Thr Lys Trp Ile Val Leu Arg Val Asp Glu Ile Asn Arg Asp
 85 90 95
 Val Ala Leu Leu Lys Tyr Val Asn Gly Thr Cys Gln Thr Thr
 100 105 110

<210> 9
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PPS1BF primer

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

<400> 9
 actcgagtct agaggattca tgaaggtgat gctttagtgg gtcg

43

<210> 10
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PPS2SR primer

<220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Introduced restriction sites

<400> 10
 gactagtgtc gacgagctct tagaatcctt caaatagatc acc

43

<210> 11
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PS1BF primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 11
gctcgagtct agaggattca tgataaatac gatcaccttt gatgctgg

48

<210> 12
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PS2SR primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 12
gactagtgtc gacgagctct taagttgtct gacaggttcc attaacg

47

<210> 13
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PS2BF primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 13
actcgagtct agaggatcca tgggagttga ttcattccct gtaaaaactg ag

52

<210> 14
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PS1SR primer

<220>

<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 14
gactagtgtc gacgagctct taagagattt ttccaatgtc actgctgag

49

<210> 15
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PSXDF primer

<220>
<221> mutation
<222> (15)..(20)
<223> Nucleotides modified to remove XbaI site

<400> 15
gctttaccca aaccacttga gctagtggat gccaaaggta cc

42

<210> 16
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PSXDR primer

<220>
<221> mutation
<222> (22)..(27)
<223> Nucleotides modified to remove XbaI site

<400> 16
gtacctttgg catccactag ctcaagtggg ttgggtaaag cc

42

<210> 17
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oryza sativa
Cystatin Delta D86 modified for potato codon usage

<400> 17
atgtcatcag acggaggacc agttttggga ggcgtcgaac cagttggaaa tgaaaatgat 60
ttgcatttgg ttgatttggc taggtttgct gttactgaac ataataaaaa agctaatagt 120

ttgttgaat ttgaaaaatt ggtagtggt aaacaacaag ttgttgetgg aactttgtac 180
tactttacta ttgaagttaa agaaggagat gctaaaaaat tgtacgaagc taaagtttgg 240
gaaaaacat ggatgtttaa agaattgcaa gaatttaaac cagttgatgc ttcagctaata 300
gcttaa 306

<210> 18
<211> 729
<212> DNA
<213> Tobacco Etch Virus

<220>
<221> mutation
<222> (382)..(387)
<223> Sequence replacing the removed SpeI site

<220>
<221> misc_feature
<222> (1)..(20)
<223> Binding site for primer NIAPROSBF

<220>
<221> misc_feature
<222> Complement((359)..(392))
<223> Binding site for primer NIAPROSDR

<220>
<221> misc_feature
<222> (397)..(411)
<223> Binding site for primer NIAPROSDF

<220>
<221> misc_feature
<222> Complement((709)..(729))
<223> Binding site for primer NIAPROSR

<400> 18
atggaaagct tgtttaaggg accacgtgat tacaaccga tatcgagcac catttgtcac 60
ttgacgaatg aatctgatgg gcacacaaca tcgttgtatg gtattggatt tgggcccttc 120
atcattacaa acaagcactt gtttagaaga aataatggaa cactgttggt ccaatcacta 180
catggtgtat tcaaggtaa gaacaccacg actttgcaac aacacctcat tgatgggagg 240
gacatgataa ttattcgcat gctaaggat tccccaccat ttctcaaaa gctgaaattt 300
agagagccac aaaggaaga gcgcataatgt cttgtgacaa ccaacttcca aactaagagc 360
atgtctagca tgggtgtcaga cacaagctgc acattccctt catctgatgg catattctgg 420
aagcattgga ttcaaaccac ggatggggcag tgtggcagtc cattagtatc aactagagat 480

ggggttcattg ttggtataca ctcagcatcg aatttcacca acacaaacaa ttatttcaca 540
 agcgtgccga aaaacttcat ggaattgttg acaaatcagg aggcgcagca gtgggttagt 600
 gggtggcgat taaatgctga ctcagtattg tggggggggcc ataaagtttt catgagcaaa 660
 cctgaagagc cttttcagcc agttaaggaa gcgactcaac tcatgagtga attggtgtac 720
 tcgcaataa 729

<210> 19
 <211> 1092
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PAP-S/Cystatin
 fusion

<220>
 <221> misc_feature
 <222> (766)..(786)
 <223> TEV NIA protease cleavage site

<220>
 <221> mutation
 <222> (681)..(686)
 <223> Modified XbaI site

<220>
 <221> misc_feature
 <222> (1)..(29)
 <223> Binding site for primer PS1BF

<220>
 <221> misc_feature
 <222> Complement((742)..(786))
 <223> Binding site for primer PCS-PAPSR

<220>
 <221> misc_feature
 <222> (766)..(806)
 <223> Binding site for primer PCS-Delta86F

<220>
 <221> misc_feature
 <222> Complement((1066)..(1092))
 <223> Binding site for primer SYNPOTDelta86SR

<400> 19
 atgataaata cgatcacctt tgatgctgga aatgccacca ttaacaaata tgccaccttt 60
 atggaatctc ttcgtaatca agcgaaagat ccaaaaactaa aatgctatgg cataccaatg 120
 ctacctgata ctaattcgac ccctaagtac ttattgggta agctccaagg tgcaaacctta 180

aaaaccatta cactaatgct gagacgaaat aacttatatcg tgatgggcta ttctgatccc 240
 ttcaatggca ataagtgtcg ttacatata tttaatgata ttacaagcac cgaacgcact 300
 gatgtggaga atactctttg ctcaagttct agttctcgtg ttgcaatgtc cattaactac 360
 aatagcttat atccgaccat ggaaaagaaa gcagaagtaa actcaagaaa tcaagtccaa 420
 ttgggaattc aaatactcag cagtgcatt ggaaaaatct ctggagttga ttcattccct 480
 gtaaaaactg aggcctttttt tctactggta gccatccaaa tggtttcaga ggcagcgcga 540
 ttcaagtaca tagagaacca agtcaagact aattttaata gagcattcta ccctgatccc 600
 aaagtaatta acttggagga gaagtggggc aaaatctctg aggcaattca caatgccaa 660
 aatggggctt tacccaaacc acttgagcta gtggatgcca aaggtaacca gtggatagtt 720
 cttagagtgg atgaaatcaa tcgtgatgtg gcactcctta agtacgaacc agtctatttc 780
 caagggatgt catcagacgg aggaccagtt ttggggaggcg tcgaaccagt tggaaatgaa 840
 aatgatttgc atttggttga tttggctagg tttgctgtta ctgaacataa taaaaaagct 900
 aatagtttgt tggaatttga aaaattggtt agtgtaaacc aacaagttgt tgctggaact 960
 ttgtactact ttactattga agttaagaa ggagatgcta aaaaattgta cgaagctaaa
 1020
 gtttgggaaa aaccatggat gtttaaagaa ttgcaagaat ttaaaccagt tgatgcttca
 1080
 gctaattgctt aa
 1092

<210> 20
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCS-PAPSR
 primer

<220>
 <221> misc_feature
 <222> (1)..(21)
 <223> TEV NIA protease cleavage site

<400> 20
 cccttggaaa tagactgggtt cgtacttaag gagtgccaca tcacg

45

<210> 21
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCS-Delta86F
primer

<220>
<221> misc_feature
<222> (1)..(21)
<223> TEV NIA protease cleavage site

<400> 21
gaaccagtct atttccaagg gatgtcatca gacggaggac c

41

<210> 22
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
SYNPOTDelta86SR primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 22
aactagtgtc gacgagctct taagcattag ctgaagcatc aactgg

46

<210> 23
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NIAPROBF
primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Introduced restriction sites

<400> 23
gctcgagtct agaggatcca tggaaagctt gtttaaggg

39

<210> 24
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NIAPROSR

<220>
<221> misc_feature
<222> (1)..(18)
<223> Introduced restriction sites

<400> 24
actagtgtcg acgagctctt attgcgagta caccaattc

39

<210> 25
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NIAPROSDF
primer

<220>
<221> mutation
<222> (6)..(11)
<223> Nucleotides modified to remove SpeI site

<400> 25
cagacacaag ctgcacattc ccttcattctg atggc

35

<210> 26
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: NIAPROSDR

<220>
<221> mutation
<222> (6)..(11)
<223> Nucleotides modified to remove SpeI site

<400> 26
gtgcagcttg tgtctgacac catgctagac atgc

34

<210> 27
<211> 381
<212> DNA
<213> Nicotiana tabacum

<400> 27
tctagaaagc ttatctaaac aaagttttaa attcatttct taaacgtcca ttacaatgta 60

atataactta gtcgtctcaa ttaaaccatt aatgtgaaat ataaatcaaa aaaagccaaa 120
 gggcggtggg acggcgccaa tcatttgtcc tagtccactc aaataaggcc catggtcggc 180
 aaaaccaaac acaaaatgtg ttattttttaa ttttttcctc ttttattgtt aaagttgcaa 240
 aatgtgttat ttttggttaag accctatgga tatataaaga caggttatgt gaaacttgga 300
 aaaccatcaa gttttaagca aaaccctctt aagaacttaa attgagcttc ttttggggca 360
 tttttctagt gagaaggatc c 381

<210> 28
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TEV NIA
 protease cleavage site (i)

<400> 28
 Glu Xaa Xaa Tyr Xaa Gln Gly
 1 5

<210> 29
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TEV NIA
 protease cleavage site (ii)

<400> 29
 Glu Xaa Xaa Tyr Xaa Gln Ser
 1 5

<210> 30
 <211> 1379
 <212> DNA
 <213> *Phytolacca americana*

<400> 30
 ctatgaagtc gggtaaagc atatacaggc tatgcattgt tagaaacatt gatgcctctg 60
 atccccgataa acaatacaaa ttagacaata agatgacata caagtaccta aactgtgtat 120
 gggggagtgga aacctcagct gctaaaaaaaa cggtgtaaga aaaaaagaaa gttgtgagtt 180
 aactacaggg cgaaagtatt ggaactagct agtaggaagg gaagatgaag tcatgcttg 240
 tggtgacaat atcaatatgg ctcatctctg caccaacttc aacttgggct gtgaatacaa 300

tcatctacaa tgttggaagt accaccatta gcaaatacgc cacttttctg aatgatcttc 360
 gtaatgaagc gaaagatcca agtttaaaat gctatggaat accaatgctg cccaatacaa 420
 atacaaatcc aaagtacgtg ttgggtgagc tccaagggtc aaataaaaaa accatcacac 480
 taatgctgag acgaaacaat ttgtatgtga tgggttattc tgatcccttt gaaaccaata 540
 aatgtcggtta ccatatcttt aatgatattc cagggtactga acgccaagat gtagagacta 600
 ctctttgccc aaatgccaat tctcgtgtta gtaaaaacat aaactttgat agtcgatatac 660
 caacattgga atcaaaagcg ggagtaaaat caagaagtca ggtccaactg ggaattcaaa 720
 tactcgacag taatattgga aagatttctg gagtgatgtc attcactgag aaaaccgaag 780
 ccgaattcct attggtagcc atacaaatgg tatcagaggc agcaagattc aagtacatag 840
 agaatcaggt gaaaactaat tttaacagag cattcaacc taatcccaa gtacttaatt 900
 tgcaagagac atggggtaag atttcaacag caattcatga tgccaagaat ggagttttac 960
 ccaaactctc cgagctagtg gatgccagtg gtgccaagtg gatagtgttg agagtggatg
 1020
 aaatcaagcc tgatgtagca ctcttaaact acgttggtgg gagctgtcag acaacttata
 1080
 accaaaatgc catgtttcct caacttataa tgtctactta ttataattac atgggttaac
 1140
 ttggtgatct atttgaagga ttctgatcat aaacataata aggagtatat atatattact
 1200
 ccaactatat tataaagctt aaataagagg ccgtgttaat tagtacttgt tgccttttgc
 1260
 tttatggtgt tgtttattat gccttgtagt cttgtaatat tatctagaga acaagatgta
 1320
 ctgtgtaata gtcttggttg aaataaaaact tccaattatg atgcaaaaaa aaaaaaaaaa
 1379

<210> 31

<211> 1378

<212> DNA

<213> *Phytolacca americana*

<400> 31

ctatgaagtc ggggtcaaagc atatacaggc tatgcattgt tagaaacatt gatgcctctg 60
 atcccgataa acaatacaaa ttagacaata agatgacata caagtaccta aactgtgtat 120
 gggggagtga aacctcagct gctaaaaaaa cggtgtaaga aaaaaagaaa gttgtgagtt 180
 aactacaggg cgaaagtatt ggaactagct agtaggaagg gaagatgaag tcaatgcttg 240
 tgggtgacaat atcaatatgg ctcatctctg caccaacttc aacttgggct gtgaatacaa 300
 tcatctacaa tgttggaagt accaccatta gcaaatacgc cacttttcgg aatgatcttc 360
 gtaatgaagc gaaagatcca agtttaaaat gctatggaat accaatgctg cccaatacaa 420

atacaaatcc aaagcacgtg ttggttgagc tccaaggttc aaataaaaaa accatcacac 480
 taatgctgag acgaaacaat ttgtatgtga tgggttattc tgatcccttt gaaaccaata 540
 aatgtcgtta ccatatcttt aatgatatct cagggtactga acgccaagat gtagagacta 600
 ctctttgccc aaatgccaat tctcgtgtta gtaaaaacat aaactttgat agtcgatatc 660
 caacattgga atcaaaagcg ggagtaaaat caagaagtca ggtccaactg ggaattcaaa 720
 tactcgacag taatattgga aagatttctg gagtgatgtc attcactgag aaaaccgaag 780
 ccgaattcct attggtagcc atacaaatgg tatcagaggc agcaagattc aagtacatag 840
 agaatcaggt gaaaactaat tttaacagag cattcaacct taatcccaa gtacttaatt 900
 tgcaagagac atggggtaag atttcaacag caattcatga tgccaagaat ggagttttac 960
 ccaaacctct cgagctagtg gatgccagtg gtgccaagtg gatagtgttg agagtggatg
 1020
 aaatcaagcc tgatgtagca ctcttaaact acgttggtgg gagctgtcag acaacttata
 1080
 accaaaatgc catgtttcct caacttataa tgtctactta ttataattac atgggttaatc
 1140
 ttggtgatct atttgaagga ttctgatcat aaacataata aggagtatat atatattact
 1200
 ccaactatat tataaagctt aaataagagg ccgtgttaat tagtacttgt tgccttttgc
 1260
 tttatgggtg tgtttattat gccttgatg cttgtaatat tatctagaga acaagatgta
 1320
 ctgtgtaata gtcttgtttg aaataaaact tccaattatg atgcaaaaaa aaaaaaaa
 1378

<210> 32
 <211> 934
 <212> DNA
 <213> *Phytolacca americana*

<400> 32
 atgaagatga aggtgttaga agtagttggg ttggcaatat cgatatggct gatgcttaca 60
 ccaccagctt cttcaaacad agtgtttgac gttgagaatg ccacaccaga aacctactct 120
 aattttctga ctagtttgcg agaagctgtg aaagacaaga aattgacatg ccatggaatg 180
 ataatggcca caaccctcac tgaacaacct aagtatgtgt tggttgacct caaattcgga 240
 tctggaacat tcacattagc aatcagaagg ggaaacttat atttggaggg ctattctgac 300
 atttacaatg gaaaatgtcg ttatcggatc ttcaaggatt cagaatccga tgccaagag 360
 accgtttgcc ccgggggacaa aagcaagcct ggcaactcaga ataatatccc ctatgaaaag 420
 agttacaaag ggatggaatc aaagggtggg gctagaacta aattaggggt aggaaagata 480
 aactcaaga gtcgaatggg taaaatctac ggcaaggatg caacggatca gaagcagtat 540

caaaaaaatg aggctgaatt tcttcttata gccgttcaaa tggttactga ggcataaagg 600
 ttcaaataca ttgagaacaa agtgaaggct aaatttgatg atgccaatgg gtatcagcca 660
 gatcctaaag ctatttcctt agagaaaaat tgggacagtg tttctaaggt cattgcaaaa 720
 gttggcacct ccggtgatag tactgttact ttacctggag acctaaaaga tgagaataat 780
 aaaccttgga ctacggccac catgaacgac cttagaacg acattatggc actcctaacc 840
 cacgttactt gcaagggttaa aagttccatg ttccttgaaa ttatgtccta ttattatagg 900
 actagtatta gtaaccttgg tgaattcgag tgat 934